Fig. 1A

```
GACGCTTCTG GGGAGTGAGG GAAGCGGTTT ACGAGTGACT TGGCTGGAGC CTCAGGGGCG GGCACTGGCA CGGAACACAC
CCTGAGGCCA GCCCTGGCTG CCCAGGCGGA GCTGCCTCTT CTCCCGCGGG TTGGTGGACC CGCTCAGTAC GGAGTTGGGG
AAGCTCTTTC ACTTCGGAGG ATTGCTCAAC AACC                       194

ATG CTG GGC ATC TGG ACC CTC CTA CCT CTG GTT CTT ACG TCT GTT GCT AGA TTA TCG TCC AAA AGT
Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala Arg Leu Ser Ser Lys Ser
                        -10                                  -1   1

GTT AAT GCC CAA GTG ACT GAC ATC AAC TCC AAG GGA TTG GAA TTG AGG AAG ACT GTT ACT ACA GTT
Val Asn Ala Gln Val Thr Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val
             10                                  20

GAG ACT CAG AAC TTG GAA GGC CTG CAT CAT GAT GGC CAA TTC TGC CAT AAG CCC TGT CCT CCA GGT
Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly
     30                                      40                                      50

GAA AGG AAA GCT AGG GAC TGC ACA GTC AAT GGG GAT GAA CCA GAC TGC GTG CCC TGC CAA GAA GGG
Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly
                                     60                                      70

AAG GAG TAC ACA GAC AAA GCC CAT TTT TCT TCC AAA TGC AGA AGA TGT AGA TTG TGT GAT GAA GGA
Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly
                             80                                      90

CAT GGC TTA GAA GTG GAA ATA AAC TGC ACC CGG ACC CAG AAT ACC AAG TGC AGA TGT AAA CCA AAC
His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro Asn
                     100     *                                110

TTT TTT TGT AAC TCT ACT GTA TGT GAA CAC TGT GAC CCT TGC ACC AAA TGT GAA CAT GGA ATC ATC
Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile
             *120                                130
```

Fig. 1B

```
AAG GAA TGC ACA CTC ACC AGC AAC ACC AAG TGC AAA GAG GAA GGA TCC AGA TCT AAC TTG GGG TGG
Lys Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
    140                                     150                                     160

CTT TGT CTT CTT CTT TTG CCA ATT CCA CTA ATT GTT TGG GTG AAG AGA AAG GAA GTA CAG AAA ACA
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys Thr
                                    170                                     180

TGC AGA AAG CAC AGA AAG GAA AAC CAA GGT TCT CAT GAA TCT CCA ACC TTA AAT CCT GAA ACA GTG
Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val
                            190                                     200

GCA ATA AAT TTA TCT GAT GTT GAC TTG AGT AAA TAT ATC ACC ACT ATT GCT GGA GTC ATG ACA CTA
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu
                    210                                     220

AGT CAA GTT AAA GGC TTT GTT CGA AAG AAT GGT GTC AAT GAA GCC AAA ATA GAT GAG ATC AAG AAT
Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn
            230                                     240

GAC AAT GTC CAA GAC ACA GCA GAA CAG AAA GTT CAA CTG CTT CGT AAT TGG CAT CAA CTT CAT GGA
Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly
    250                                     260                                     270

AAG AAA GAA GCG TAT GAC ACA TTG ATT AAA GAT CTC AAA AAA
Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys
                                    280
```

Fig. 2A

```
1100                                                                        1150
GCC AAT CTT TGT ACT CTT GCA GAG AAA ATT CAG ACT ATC ATC CTC AAG GAC ATT ACT AGT GAC TCA
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser
                    290                                     300

                                                   1200
GAA AAT TCA AAC TTC AGA AAT GAA ATC CAA AGC TTG GTC TAG AGTGAAAAACAACAAATTCAGTTCTGA
Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val End
            310                                 319

               1250                                                     1300
GTATATGCAATTAGTGTTTGAAAAGATTCTTAATAGCTGGCTGTAAATACTGCTTGGTTTTTACTGGGTACATTTTATC

                                  1350
ATTTATTAGCGCTGAAGAGCCAACATATTTGTAGATTTTTAATATCTCATGATTCTGCCTCCAAGGATGTTTAAAATCTA

     1400                                                     1450
GTTGGGAAAACAAACTTCATCAAGAGTAAATGCAGTGGCATGCTAAGTACCCAAATAGGAGTGTATGCAGAGGATGAAAG

                         1500                                                   1550
ATTAAGATTATGCTCTGGCATCTAACATATGATTCTGTAGTATGAATGTAATCAGTGTATGTTAGTACAAATGTCTATCC

                                                  1600
ACAGGCTAACCCCACTCTATGAATCAATAGAAGAAGCTATGACCTTTTGCTGAAATATCAGTTACTGAACAGGCAGGCCA

               1650                                                       1700
CTTTGCCTCTAAATTACCTCTGATAATTCTAGAGATTTTACCATATTTCTAAACTTTGTTTATAACTCTGAGAAGATCAT

                                  1750
ATTTATGTAAAGTATATGTATTTGAGTGCAGAATTTAAATAAGGCTCTACCTCAAAGACCTTTGCACAGTTTATTGGTGT
```

Fig. 2B

1800 1850
CATATTATACAATATTTCAATTGTGAATTCACATAGAAAACATTAAATTATAATGTTTGACTATTATATATGTGTATGCA

1900 1950
TTTTACTGGCTCAAAACTACCTACTTCTTTCTCAGGCATCAAAAGCATTTTGAGCAGGAGAGTATTACTAGAGCTTTGCC

2000
ACCTCTCCATTTTTGCCTTGGTGCTCATCTTAATGGCCTAATGCACCCCCAAACATGGAAATATCACCAAAAAATACTTA

2050 2100
ATAGTCCACCAAAAGGCAAGACTGCCCTTAGAAATTCTAGCCTGGTTTGGAGATACTAACTGCTCTCAGAGAAAGTAGCT

2150
TTGTGACATGTCATGAACCCATGTTTGCAATCAAAGATGATAAAATAGATTCTTATTTTTCCCCCACCCCCGAAAATGTT

2200 2250
CAATAATGTCCCATGTAAAACCTGCTACAAATGGCAGCTTATACATAGCAATGGTAAAATCATCATCTGGATTTAGGAAT

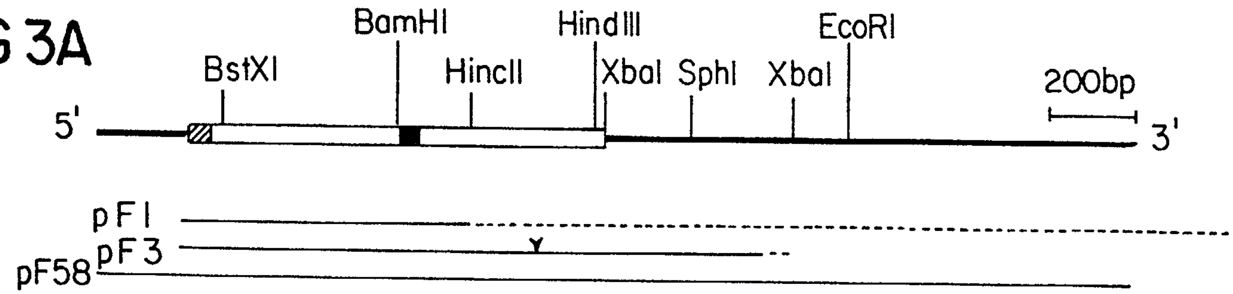
2300 2350
TGCTCTTGTCATACCCTCAAGTTTCTAAGATTTAAGATTCTCCTTACTACTATCCTACGTTTAAATATCTTTGAAAGTTT

2400
GTATTAAATGTGAATTTTAAGAAATAATATTTATATTTCTGTAAATGTAAACTGTGAAGATAGTTATAAACTGAAGCAGA

2450 2500
TACCTGGAACCACCTAAAGAACTTCCATTTATGGAGGATTTTTTGCCCCTTGTGTTTGGAATTATAAAATATAGGTAAA

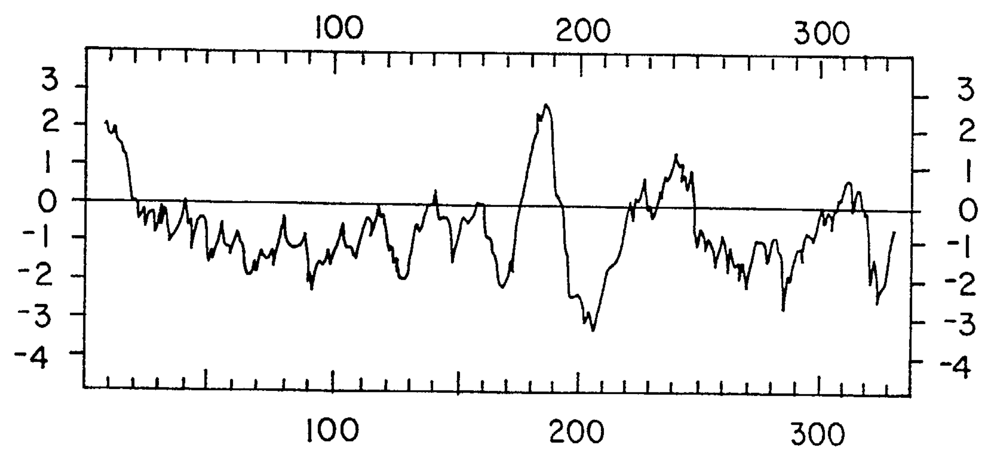
AGTACGTAATTAAATAATGTTTTTG

FIG 3A



BamHI
HindIII
EcoRI
BstXI
HincII
XbaI
SphI
XbaI
200bp
5'
3'
pF1
pF3
pF58

FIG 3B



100
200
300
3
2
1
0
-1
-2
-3
-4

FIG. 4A

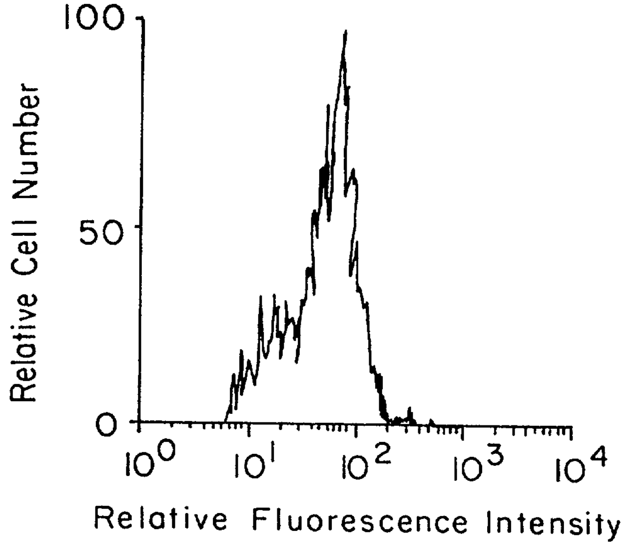

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 4B

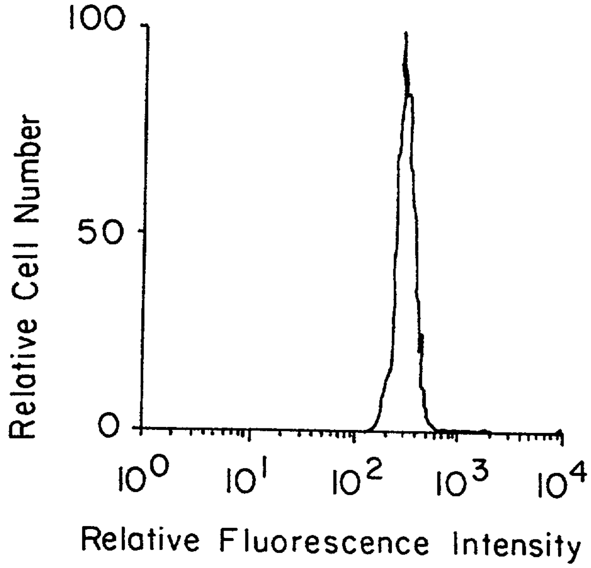

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 4C

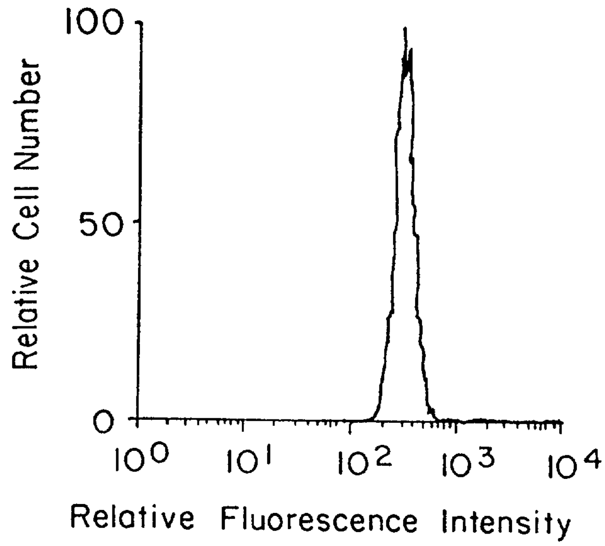

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 4D

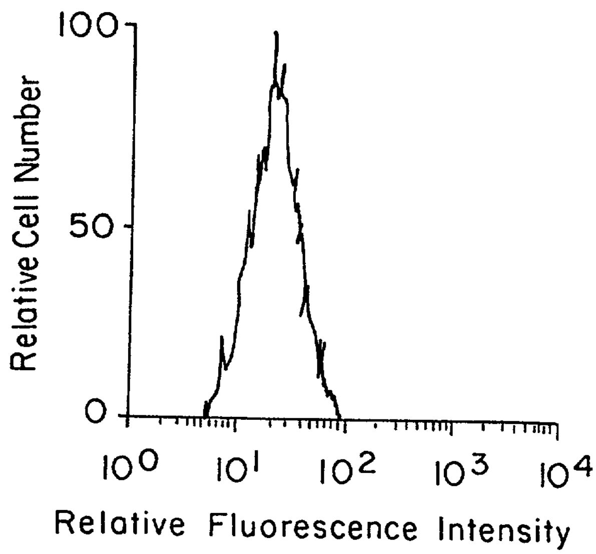

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 4E

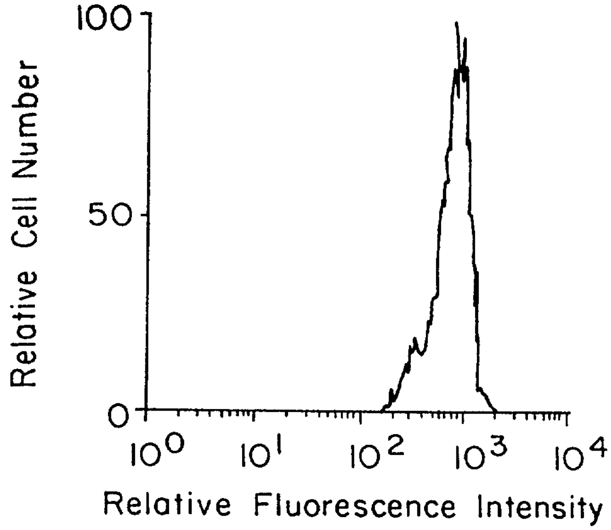

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 4F

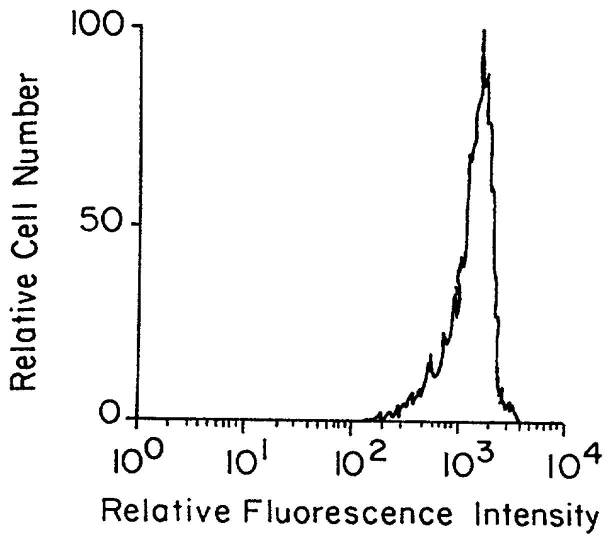
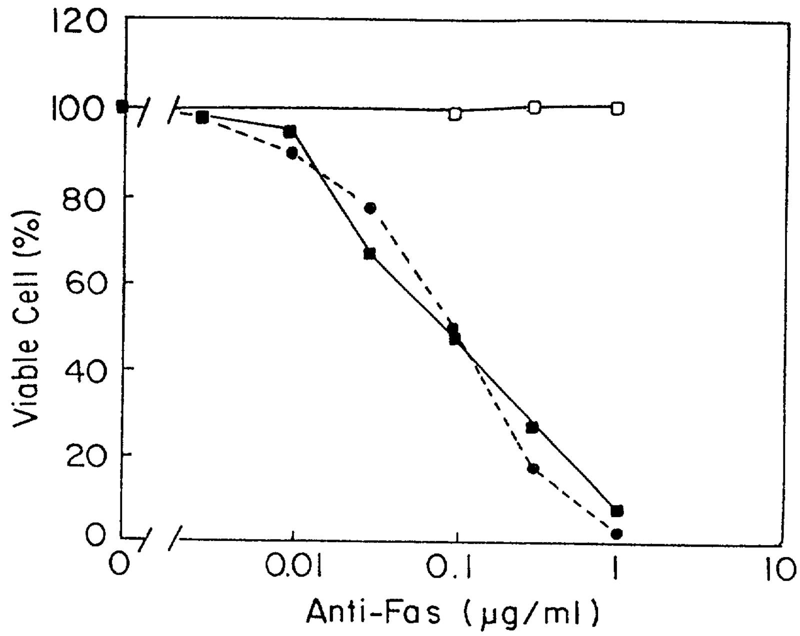
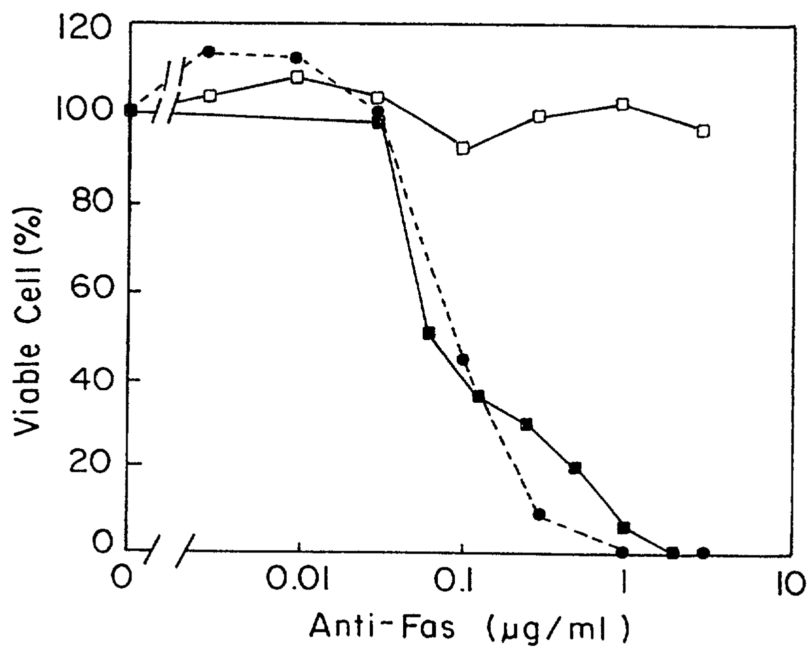

100
50
0
Relative Cell Number
10^0 10^1 10^2 10^3 10^4
Relative Fluorescence Intensity

FIG. 5



120
100
80
60
40
20
0
Viable Cell (%)
0
0.01
0.1
1
10
Anti-Fas (μg/ml)

FIG. 6



120
100
80
60
40
20
0
Viable Cell (%)
0
0.01
0.1
1
10
Anti-Fas (μg/ml)

FIG.7

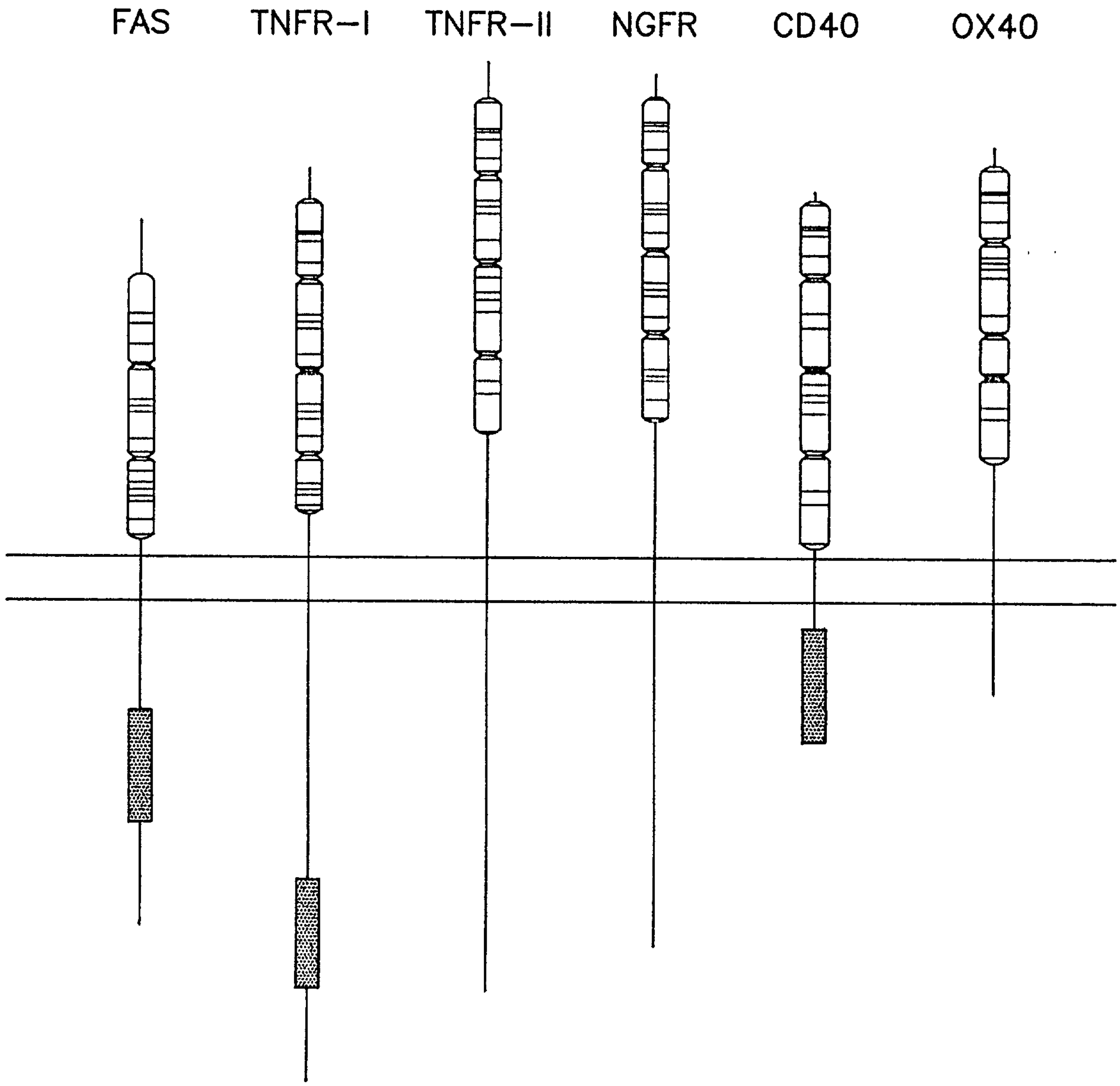


Fig. 8A

hFAS	(31-67)	Q	N	L	E	G	L	H	-	H	D	G	Q	F	-	-	-	-	-	-	C	H	-	K
hTNFR1	(3-42)	V	C	P	Q	G	K	Y	I	H	P	Q	N	N	-	-	-	-	S	I	C	C	-	T
hTNFR2	(39-76)	T	C	R	L	R	E	Y	Y	D	-	Q	T	A	-	-	-	-	Q	M	C	C	-	S
hNGFR	(3-37)	A	C	P	T	G	L	Y	T	H	S	G	E	-	-	-	-	-	-	-	C	C	-	K
hCD40	(25-60)	A	C	R	E	K	Q	Y	L	I	N	S	Q	-	-	-	-	-	-	-	C	C	-	S
rOX40	(25-60)	N	C	V	K	D	T	Y	P	S	G	H	K	-	-	-	-	-	-	-	C	C	-	R
hFAS	(68-112)	P	C	Q	E	G	K	E	Y	T	D	K	A	H	F	S	S	K	C	R	R	C	-	R
hTNFR1	(43-86)	E	C	E	S	G	S	F	T	A	S	E	N	H	L	-	R	H	C	L	S	C	-	S
hTNFR2	(77-119)	S	C	E	D	S	T	Y	T	Q	L	W	N	W	V	-	P	E	C	L	S	C	G	S
hNGFR	(38-80)	P	C	L	D	S	V	T	S	S	D	V	V	S	A	I	E	P	C	K	P	C	-	T
hCD40	(61-104)	P	C	G	E	S	E	F	L	D	T	W	N	R	E	I	H	-	C	H	Q	H	-	K
rOX40	(61-103)	P	C	-	E	P	G	F	Y	N	E	A	V	N	Y	-	D	T	C	K	Q	C	-	T
hFAS	(113-149)	-	C	K	P	N	F	F	C	N	-	-	S	T	V	C	E	H	C	D	P	C	-	-
hTNFR1	(87-126)	-	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	I	E	Q	C	F	N	C	-	-
hTNFR2	(120-162)	-	C	R	P	G	W	Y	C	A	-	-	L	S	K	Q	E	G	C	R	L	C	A	P
hNGFR	(81-119)	-	C	A	Y	G	Y	Y	Q	D	-	-	-	E	T	I	G	R	C	E	A	C	-	-
hCD40	(105-144)	-	C	E	E	G	W	H	C	-	-	-	-	-	T	S	E	A	C	E	S	C	V	L
rOX40	(104-123)	-	C	R	P	G	T	Q	P	-	-	-	-	-	R	Q	D	S	-	-	-	-	-	-
hTNFR1	(127-155)	T	C	H	A	G	F	F	L	R	-	-	E	N	E	-	-	-	C	V	S	C	-	S
hTNFR2	(163-201)	P	C	A	P	G	T	F	S	N	T	T	S	S	T	-	D	I	C	R	P	H	-	Q
hNGFR	(120-161)	E	C	P	D	G	T	Y	S	D	E	A	N	H	V	-	D	P	C	L	P	C	-	T
hCD40	(145-186)	P	C	P	V	G	F	F	S	N	V	S	S	A	F	-	E	K	C	H	P	-	-	T
rOX40	(124-164)	P	C	P	P	G	H	F	S	P	G	S	N	Q	-	-	-	A	C	K	P	W	-	T
Consensus			C			G		Y											C			C		
						S		F																

Fig. 8B

P	C	P	P	G	E	R	K	A	R	D	-	-	C	T	V	N	G	D	E	P	D	C	V
K	C	H	K	G	T	Y	L	Y	N	D	-	-	C	P	G	P	G	Q	D	T	D	C	R
K	C	S	P	G	Q	H	A	K	V	F	-	-	C	T	K	T	S	-	D	T	V	C	D
A	C	N	L	G	E	G	V	A	Q	P	-	-	C	G	A	-	-	N	Q	T	V	C	E
L	C	Q	P	G	Q	K	L	V	S	D	-	-	C	T	E	F	-	T	E	T	E	C	L
E	C	Q	P	G	H	G	M	V	S	R	-	-	C	D	H	T	-	R	D	T	V	C	H
L	C	D	E	G	H	G	L	E	V	E	I	N	C	T	R	T	-	Q	N	T	K	C	R
K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D	-	R	D	T	V	C	G
R	C	S	D	D	-	-	Q	V	E	T	Q	A	C	T	R	E	-	Q	N	R	I	C	T
E	C	V	G	L	Q	S	M	S	A	P	-	-	C	V	E	A	-	D	D	A	V	C	R
Y	C	D	P	N	L	G	L	R	V	Q	Q	K	G	T	S	E	-	T	D	T	I	C	T
Q	C	N	H	R	S	G	S	E	L	K	Q	N	C	T	P	T	-	E	D	T	V	C	Q
-	T	K	C	E	H	G	I	-	I	K	E	-	C	T	L	T	-	S	N	T	K	C	-
-	S	L	C	L	N	G	T	-	V	H	L	S	C	Q	E	K	-	Q	N	T	V	C	-
L	R	K	C	R	P	G	F	G	V	A	R	P	G	T	E	T	-	S	D	V	V	C	K
-	R	V	C	E	A	G	S	G	L	V	F	S	C	Q	D	K	-	Q	N	T	V	C	E
H	R	S	C	S	P	G	F	G	V	K	Q	I	A	T	G	V	-	S	D	T	I	C	E
-	-	-	-	S	H	K	F	G	V	D	-	-	-	-	-	-	-	-	-	-	-	C	V
N	C	K	K	S	L	-	-	-	-	-	-	E	C	T	K	-	-	-	-	-	L	C	-
I	C	N	-	-	-	-	V	V	A	-	-	I	P	G	N	A	S	M	D	A	V	C	T
V	C	E	D	T	E	R	Q	L	R	-	-	E	C	T	R	W	-	A	D	A	E	C	E
S	C	E	T	K	D	L	V	V	Q	-	-	Q	A	G	T	N	K	T	D	V	V	C	G
N	C	T	L	S	G	K	Q	I	R	-	-	H	P	A	S	N	S	L	D	T	V	C	E
	C												C	T					D	T	V	C	
																			N				

Fig 9

hCD40 (225-247)	K	A	P	H	P	K	Q	E	P	Q	E	I	N	F	P	D	D	L	P	G	S	N	T
hFAS (230-251)	K	G	F	V	R	K	N	G	V	N	E	A	K	I	-	D	E	I	K	N	D	N	V
hTNFRI (332-353)	K	E	F	V	R	R	L	G	L	S	D	H	E	I	-	D	R	L	E	L	Q	N	G

hCD40 (248-269)	A	A	P	V	Q	E	T	L	H	G	C	Q	P	V	E	Q	E	D	G	-	K	E	S
hFAS (252-274)	Q	D	T	A	E	Q	K	V	Q	L	L	R	N	W	E	Q	L	H	G	K	K	E	A
hTNFRI (354-376)	R	C	L	R	E	A	Q	Y	S	M	L	A	T	W	R	R	R	T	P	R	R	E	A